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The validity of *Rana bannanica* Rao & Yang, 1997 (Anura, Ranidae)

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Abstract

One specimen of frog was collected from Mohan Town, Mengla County, Xishuangbanna Prefecture, Yunnan Province, China, which is the type locality of *Rana bannanica* Rao & Yang, 1997, currently considered as a junior synonym of *Hylarana milleti* (Smith, 1921). This specimen well agrees with the original description of *R. bannanica*. In regard to morphology, *R. bannanica* and *H. milleti* are, indeed, very similar, but can still be distinguished from each other. Phylogenetic analysis, based on mitochondrial gene sequences, showed that this specimen and *H. milleti* are different species. Hence, we remove *R. bannanica* from the synonymy of *H. milleti*.

Key Words

16S, COI, cytb, *Hylarana milleti*, resurrection, synonym, systematics, taxonomy

Introduction

The systematics and taxonomy of Golden-backed frogs of the genus *Hylarana* Tschudi, 1838 have long been chaotic (Dubois 1992; Oliver et al. 2015; Chan et al. 2020; Dubois et al. 2021; Reilly et al. 2022). Previously, it had been divided into 10 genera, namely *Hylarana*, *Hydrophylax* Fitzinger, 1843, *Amnirana* Dubois, 1992, *Chalcorana* Dubois, 1992, *Humerana* Dubois,1992, *Papurana* Dubois, 1992, *Pulchrana* Dubois, 1992, *Sylvirana* Dubois, 1992, *Abavorana* Oliver, Prendini, Kraus & Raxworthy, 2015, and *Indosylvirana* Oliver, Prendini, Kraus & Raxworthy, 2015 (Oliver et al. 2015; Chan et al. 2020). Later, except for *Abavorana*, the other nine genera were placed back into *Hylarana*, relegating those ranks as subgenera (Dubois et al. 2021; Reilly et al. 2022). At present, the website Amphibian Species of the World (https://amphibiansoftheworld.amnh.org/) also adopts this viewpoint (Frost 2023).

Rana bannanica Rao & Yang, 1997 is a poorly-known ranid species described in 1997 from Xishuangbanna Prefecture, Yunnan Province, China and its type locality is in Mohan Town, Mengla County, Xishuangbanna Prefecture, Yunnan Province, China, close to the border with Laos (Rao and Yang 1997). Since this species was described, there have been no formal collection reports of this species from its type locality.

Rana milleti Smith, 1921 was described from the Langbian Plateau, Lam Dong Province, central-southern

Vietnam and, subsequently, this species was reported from Thailand and Cambodia (Chuaynkern et al. 2004; Stuart and Emmett 2006). Thereafter, Ohler (2007) proposed *R. bannanica* as a junior synonym of *R. milleti* by morphological data, based on several specimens collected from Phongsaly, Laos, as she considered that these specimens resemble both *R. bannanica* and *R. milleti*.

Currently, *Rana milleti* is regarded as *Hylarana milleti* and considered to be distributed in Vietnam, Thailand, Cambodia, Laos, southern China and peninsular Myanmar and *R. bannanica* is considered to be a synonym of *H. milleti* (Ohler 2007; Chan et al. 2020; Poyarkov et al. 2021; Zug 2022).

During our field surveys in Yunnan Province, China and in southern Vietnam from 2019 to 2023, we collected one frog specimen from the type locality of *Rana bannanica*, Xishuangbanna and six specimens of *Hylarana milleti* from its type locality, Langbian Plateau, Lam Dong Province (Fig. 1). We collected molecular sequence data of these specimens in order to reconstruct a molecular phylogeny and evaluate the phylogenetic position of them. Our phylogenetic analysis of molecular data demonstrated that the specimen from Xishuangbanna and the specimens from Langbian Plateau are not the same species. Thus, we resurrect *R. bannanica* and re-assess its taxonomic status.

Materials and methods

The specimen from China was collected from Manzhuang Village, Mohan Town, Mengla County, Xishuangbanna Prefecture, Yunnan Province and the specimens from Vietnam were collected from Da Lat and Di Linh, Lam Dong Province. Liver or muscular tissue samples were preserved in 99% ethanol for molecular analysis. The specimen from China was deposited in Kunming Institute of Zoology, Chinese Academy of Sciences (KIZ) and the specimens from Vietnam were deposited in Zoological Museum of Moscow University (ZMMU).

Measurements were taken with a digital calliper to the nearest 0.1 mm. We measured: snout-vent length (SVL), head length (HL), head width (HW), snout length (SL), eye diameter (ED), interorbital distance (IND), tympanum diameter (TD), forearm and hand length (FHL), total arm length (ARM), tibia length (TL), tarsus and foot length (TFL), foot length (FL) and total leg length (LEG).

Total genomic DNA was extracted from liver or muscular tissues. A fragment of the 16S rRNA (16S) gene was amplified and sequenced using the primers L2188: 5'–AAAGTGGGCCTAAAAGCAGCCA–3' and 16H1: 5'–CTCCGGTCTGAACTCAGATCAC-

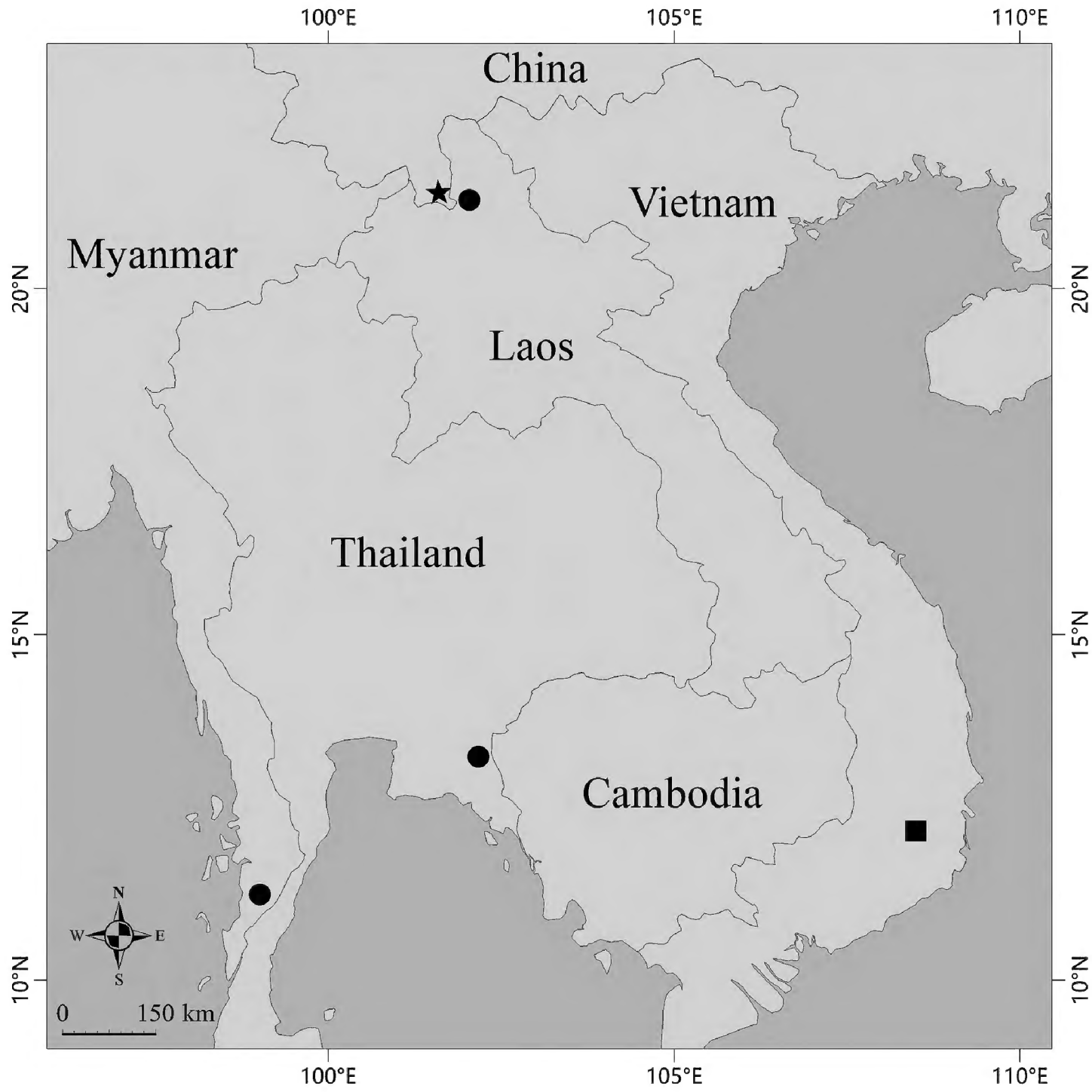

Figure 1. Map showing the type locality (black star) of *Hylarana bannanica* in Xishaungbanna, Yunnan, China and the type locality (black square) of *H. milleti* in Langbian Plateau, Lam Dong, Vietnam and other confirmed distributions (black dots) of *H. bannanica* in Phongsaly, Laos, Chanthaburi, Thailand and Tanintharyi, Myanmar, respectively, based on molecular data.

GTAGG–3' (Hedges 1994; Matsui et al. 2006), a fragment of the cytochrome c oxidase subunit I (COI) gene was amplified and sequenced using the primers Chmf4: 5'–TYTCWACWAAYCAYAAAGAYATCGG–3' and Chmr4: 5'–ACYTCRGGRTGRCCRAARAATCA–3' (Che et al. 2012) and a fragment of the cytochrome b (cytb) gene was amplified and sequenced using the primers cytb-c: 5'–CTACTGGTTGTCCTCCGATTCATGT–3' and CB-J-10933: 5'–TATGTTCTACCATGAGGACAAATATC–3' (Bossuyt and Milinkovitch 2000). All new sequences have been deposited in GenBank. Other sequences were obtained from GenBank (Table 1).

Sequences were aligned using MAFFT 7.471 (Katoh and Standley 2013) with default parameters. Phylogenetic analyses were constructed, based on the concatenated sequences of 16S, COI and cytb genes. The best fit models were selected using the corrected Akaike Information Criterion (AICc) in ModelFinder which was implemented in IQ-TREE 1.6.12 (Kalyaanamoorthy et al. 2017). Bayesian Inference (BI) was performed in MrBayes 3.2.7 (Ronquist et al. 2012), based on the GTR+F+I+G4 substitution model for all partitions and the Markov chains were run for 5,000,000 generations and sampled every 100 generations. Maximum Likelihood (ML) analysis was performed in IQ-TREE 1.6.12 (Nguyen et al. 2015), based on the GTR+F+R4 substitution model for 16S, the TIM2+F+I+G4 substitution model for COI and the TVM+F+I+G4 substitution model for cytb and branch support was assessed using 1,000 ultrafast bootstrap replicates.

Table 1. Sequences used in this study.

Species	Voucher	16S	COI	cytb
Abavorana luctuosa	FMNH 273219	KR264088	–	KR264180
Hylarana albolabris	MVZ 234147	JX564871	JX564871	JX564871
Hylarana amnicola	USNM 584214	KY080042	KY079510	–
Hylarana annamitica	AMNH A-161290	MG606336	–	–
Hylarana arfaki	BPBM19463	KR264048	–	KR264139
Hylarana asperrima	AMNH 117606	MG552350	–	–
Hylarana attigua	FMNH 258259	MG606313	–	–
Hylarana aurantiaca	BNHS 5813	KM068913	KM069020	KM069128
Hylarana aurata	RG6548	KR264101	–	KR264192
Hylarana bahuvistara	BNHS 5921	KT281144	–	–
Hylarana bannanica	KIZ2019BN	PP034378	PP050559	PP035221
Hylarana bannanica	0281Y	KR827825	KR087730	–
Hylarana bannanica	2004.0373	KR827824	KR087729	–
Hylarana bannanica	2004.0375	KR827823	KR087728	–
Hylarana bannanica	USNM 594329	MT608886	MT608217	–
Hylarana bannanica	USNM 594330	MT608885	MT608216	–
Hylarana baramica	BNP024	DQ835348	–	–
Hylarana caesari	BNHS 5842	KM068915	KM069022	KM069130
Hylarana centropeninsularis	DWNP1189	EU604198	–	–
Hylarana chalconota	MVZ 239431	KR264095	–	KR264187
Hylarana cubitalis	2005.0228	KR827781	KR087688	–
Hylarana daemeli	BPBM36025	KR264057	–	KR264148
Hylarana darlingi	PEMA6989	KR264121	–	KR264208
Hylarana doni	BNHS 5819	KM068928	KM069035	KM069143
Hylarana elberti	USNM 579404	OL960068	–	–
Hylarana erythraea	USNM 587708	MT608883	MT608214	–
Hylarana eschatia	USNM 587721	MT608717	MT608044	–
Hylarana faber	2003.0419	KR827801	KR087706	–
Hylarana flavescens	BNHS 5845	KM068931	KM069038	KM069146
Hylarana florensis	MVZ 292869	OL960058	–	–
Hylarana fonensis	ZMBMH0145	MG552337	–	–
Hylarana galamensis	MVZ 245225	KR264096	–	KR264188
Hylarana garritor	BPBM15488	KR264042	–	KR264133
Hylarana glandulosa	KUHE 53618	AB719223	–	–
Hylarana gracilis	DZ 1173	KM068939	KM069046	KM069154
Hylarana grandocula	PNM 7588	KP298046	–	–
Hylarana guentheri	LC2018092202	MN248533	MN248533	MN248533
Hylarana humeralis	USNM 583171	MG935823	MG935527	–
Hylarana indica	BNHS 5856	KM068951	KM069058	KM069165
Hylarana intermedia	BNHS 5831	KM068960	KM069067	KM069174
Hylarana jimiensis	BPBM22832	KR264053	–	KR264144
Hylarana krefftii	–	KM247362	KM247362	KM247362
Hylarana lacrima	USNM 583124	MG935997	MG935703	–
Hylarana lateralis	MBM-JBS19852	MG935831	MG935537	–

Species	Voucher	16S	COI	cytb
Hylarana laterimaculata	KUHE 17594	AB719229	–	–
Hylarana latouchii	LSU20200422001ZL	MT702387	MT702387	MT702387
Hylarana leptoglossa	ZHRAB	OR058745	OR058745	OR058745
Hylarana lepus	USNM 584215	KY080044	KY079512	–
Hylarana longipes	CAS 254205	MG552472	–	–
Hylarana macrodactyla	0095Y	KR827808	KR087713	–
Hylarana magna	BNHS 5857	KM068964	KM069071	KM069178
Hylarana malabarica	BNHS 5880	KM068968	KM069075	KM069182
Hylarana malayana	USNM 587709	MT609321	MT608642	–
Hylarana maosonensis	K742	KR827809	KR087714	–
Hylarana megalonesa	FMNH 268981	KR264085	–	KR264176
Hylarana melanomenta	ELR165	KF477693	–	–
Hylarana milleti	ZMMU NAP-12372	PP034384	–	–
Hylarana milleti	ZMMU NAP-12373	PP034383	–	–
Hylarana milleti	ZMMU NAP-12374	PP034382	–	–
Hylarana milleti	ZMMU NAP-12862	PP034381	–	–
Hylarana milleti	ZMMU NAP-12863	PP034380	–	–
Hylarana milleti	ZMMU NAP-12864	PP034379	–	–
Hylarana milleti	DL35	OR095101	–	–
Hylarana milleti	DL38	OR095092	–	–
Hylarana milleti	DL40	OR095093	–	–
Hylarana milleti	DL51	OR095094	–	–
Hylarana milleti	ROM 34429	KR264108	–	KR264199
Hylarana cf. *milleti*	ROM 7240	AF206490	–	–
Hylarana milneana	BPBM15749	KR264044	–	KR264135
Hylarana miopus	0313Y	KR827778	KR087686	–
Hylarana montana	BNHS 5866	KM068978	KM069085	KM069192
Hylarana montosa	NCSM 76398	MG606619	–	–
Hylarana mortenseni	FMNH 263303	KR264076	–	KR264166
Hylarana nigrovittata	USNM 583176	MG936001	MG935707	–
Hylarana papua	LSUMZ97639	KR264091	–	KR264183
Hylarana parvaccola	FMNH 268599	EF487450	–	–
Hylarana raniceps	FMNH 267958	DQ650408	–	–
Hylarana roberti	CAS 243913	MG606593	–	–
Hylarana rufipes	FMNH268575	KR264081	–	KR264172
Hylarana serendipi	DZ 1145	KM068980	KM069087	KM069194
Hylarana siberu	BJE203	KF477742	–	–
Hylarana signata	FMNH 273117	KR264086	–	KR264178
Hylarana similis	KU 306511	KF477775	–	–
Hylarana spinulosa	MVZ 236683	KR264093	–	KR264185
Hylarana sreeni	BNHS 5872	KM068994	KM069102	KM069208
Hylarana supragrisea	BPBM24218	KR264055	–	KR264146
Hylarana taipehensis	USNM 595412	OM387135	OM420406	–
Hylarana temporalis	DZ 1092	KM068995	KM069103	KM069209
Hylarana tytleri	USNM 583137	MG935833	MG935539	–
Hylarana urbis	BNHS 5841	KM069008	KM069116	KM069221
Hylarana volkerjane	RG7636	KR264104	–	KR264195
Hylarana waliesa	BPBM16384	KR264046	–	KR264137

Results

Morphologically, the specimen from the type locality of *Rana bannanica* well agrees with the original description of *R. bannanica* in that all measurements and the relative lengths of body parts of this specimen are within the ranges of those in the type series of *R. bannanica* (n = 8) (Table 2). Therefore, we consider this specimen to belong to the species described by Rao and Yang (1997). However, the ratio of head width to head length in males of *R. bannanica* (n = 9) is relatively smaller than that in males of *H. milleti* (n = 5) (HW/HL 0.31–0.35 vs. 0.35–0.36), the ratio of snout length to snout-vent length in males of *R. bannanica* is relatively larger than that in males of *H. milleti* (SL/SVL 0.17–0.18 vs. 0.15–0.17) and the ratio of total leg length to snout-vent length in males of *R. bannanica* is relatively smaller than that in males of *H. milleti* (LEG/SVL 1.53–1.69 vs. 1.70–1.78) (Table 2). In addition, *R. bannanica* differs from *H. milleti* by having relatively larger discs on tips of fingers and toes, having relatively larger outer metatarsal tubercle, having tarsal folds and having vocal sacs in males.

In phylogenetic analyses of mtDNA sequences, BI and ML methods yielded similar results. The newly-generated sequences of *Hylarana milleti*, as well as the sequences of the specimens of *H. milleti* from Lam Dong and Gia Lai

Table 2. Morphological comparison between the type and topotypic specimens of *Hylarana bannanica* and the type specimens of *H. milleti*. Data for the type specimens of *H. bannanica* and *H. milleti* were obtained from the original descriptions by Rao and Yang (1997) and Smith (1921), respectively.

	Hylarana bannanica **n = 8** ♂ **Holotype and paratypes**	***Hylarana bannanica*** **n = 1 (KIZ2019BN)** ♂ **Topotype**	***Hylarana milleti*** **n = 5** ♂ **Syntypes**	***Hylarana milleti*** **n = 5** ♀ **Syntypes**
SVL	38.0–43.0	40.4	36–39	45–48
HL	10.5–17.0	16.2	14–14.5	16–17
HW	12.0–14.0	13.5	12.5–14	15–16
HL/SVL	0.28–0.44	0.40	0.36–0.39	0.33–0.37
HW/SVL	0.31–0.35	0.33	0.35–0.36	0.31–0.35
HW/HL	0.76–1.14	0.83	0.89–1.00	0.94
SL	7.0–7.5	6.8	6	7–8
SL/HL	0.41–0.67	0.42	0.41–0.43	0.41–0.47
SL/SVL	0.17–0.18	0.17	0.15–0.17	0.15–0.17
ED	/	5.0	4–4.5	5
ED/HL	/	0.31	0.29–0.32	0.29–0.31
ED/SVL	/	0.12	0.10–0.13	0.10–0.11
IND	3.8–4.2	3.9	3–4	4–5
TD	4.1–5.0	4.1	3.4–4	4
TD/HL	0.25–0.43	0.25	0.24–0.29	0.24–0.25
TD/SVL	0.10–0.12	0.10	0.09–0.11	0.08–0.09
FHL	18–20	19.2	/	/
ARM	/	25.2	21–24	27–29
TL	19.8–23.0	21.2	20–21	25–27
TL/SVL	0.52–0.56	0.52	0.54–0.56	0.53–0.60
TFL	29.0–33.0	32.7	/	/
FL	20.0–23.0	22.9	20–21	25–27
FL/SVL	0.51–0.58	0.57	0.54–0.56	0.53–0.58
LEG	58–67	68.2	62–67	79–85
LEG/SVL	1.53–1.69	1.69	1.70–1.78	1.49–1.80

provinces in Vietnam and the newly-generated sequence of the specimen from the type locality of *Rana bannanica*, as well as the sequences of the specimens previously identified under the name *H. milleti* from Phongsaly Province in Laos, Chanthaburi Province in Thailand and Tanintharyi Region in Myanmar, formed two distant, separate clades within the genus *Hylarana* (Fig. 2). Clearly, the specimens previously considered to be *H. milleti* from China, Laos, Thailand and Myanmar and the specimens of *H. milleti* from Vietnam belong to different species, although their phylogenetic positions within the genus have not been resolved. Therefore, we formally remove *Rana bannanica* Rao & Yang, 1997 from the synonym of *Hylarana milleti* Smith, 1921.

Hylarana bannanica (Rao & Yang, 1997)

Figs 3, 4, 5A

Rana bannanica Rao & Yang, 1997.

Type material. ***Holotype.*** KIZ 94001, adult male. ***Paratypes.*** KIZ 94002–KIZ 94008, seven adult males.

Type locality. Mohan Town, Mengla County, Xishuangbanna Prefecture, Yunnan Province, China.

Specimen examined. KIZ2019BN, adult male, collected by Shuo Liu from Manzhuang Village, Mohan Town, Mengla County, Xishuangbanna Prefecture, Yunnan Province, China (21°21'51"N, 101°37'17"E, 760 m elevation), on 7 May 2019.

Description of the newly-collected topotypic specimen. SVL 40.4 mm; head width less than head length (HW/HL 0.83); snout pointed, projecting beyond lower jaw; nostril slightly closer to snout than to eye; canthus rostralis distinct; loreal region vertical, slightly concave; snout length greater than eye diameter; pineal body indistinct; tympanum relatively large (TD/ED 0.82), rounded; vomerine teeth distinct; choanae close to vomerine teeth; tongue oval, posterior notch U-shaped; vocal sac openings small, on floor of each corner of mouth; vocal sacs present.

Forelimbs relatively slender; relative lengths of fingers III > I ≥ IV > II; all finger tips expanded into small discs; webbing on fingers absent; subarticular tubercles distinct, oval and prominent; supernumerary tubercles below base of fingers II–IV present, small and rounded; thenar tubercle oval, large; median metacarpal tubercle oval, prominent; outer metacarpal tubercle elongated, indistinct; grey nuptial pad on finger I indistinct.

Hind limbs medium long; relative lengths of toes IV > V > III > II > I; all toe tips expanded into small discs, discs on toes slightly larger than on fingers; webbing on toes undeveloped; subarticular tubercles distinct, oval, prominent; inner metatarsal tubercle oval; outer metatarsal tubercle rounded; tarsal fold present.

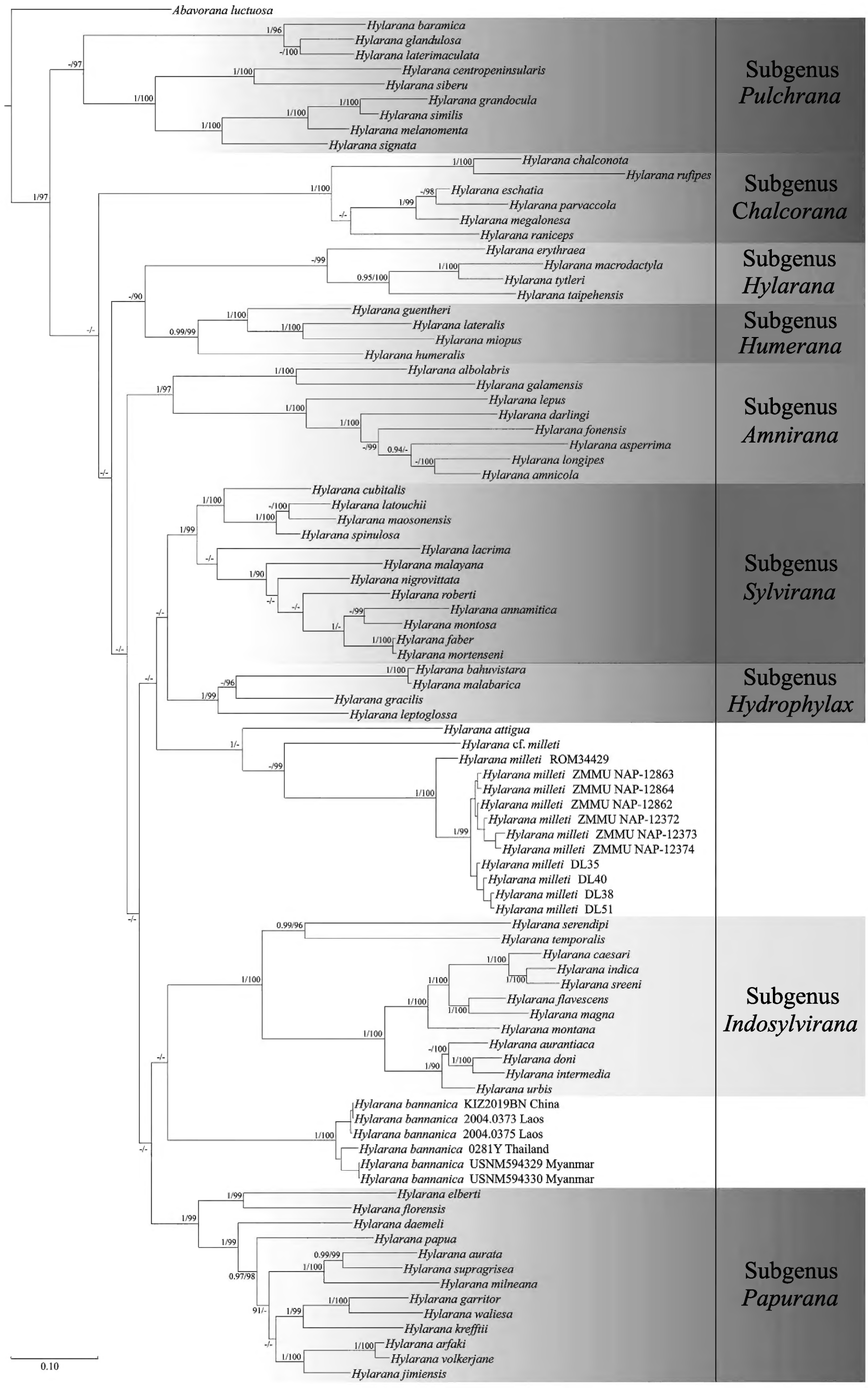

Figure 2. Bayesian phylogenetic tree of *Hylarana* inferred from the concatenated 16S, COI and cytb sequences. Numbers before slashes indicate Bayesian posterior probabilities (≥ 0.90) and numbers after slashes indicate ML bootstrap supports (≥ 90).

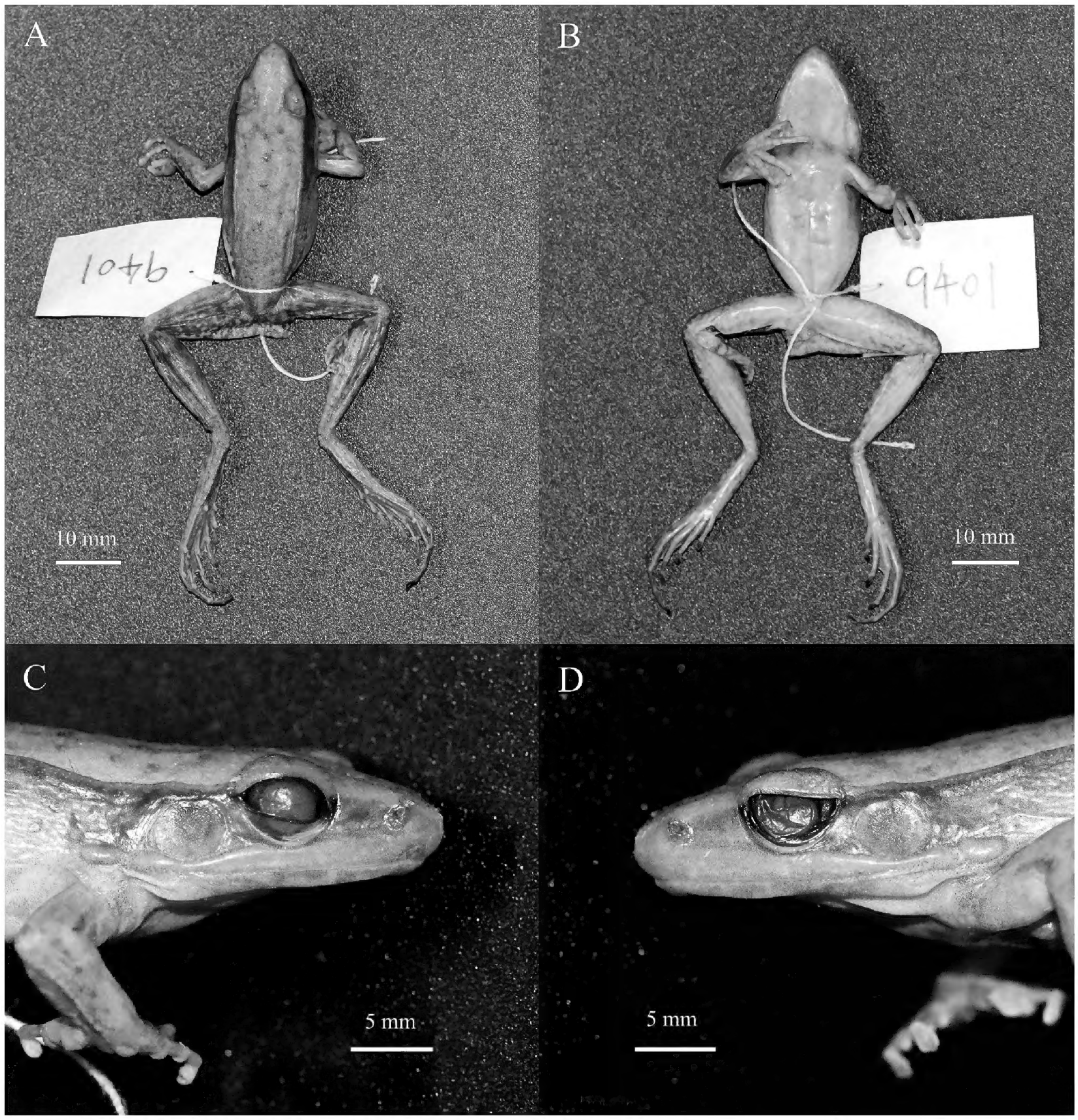

Figure 3. The holotype (KIZ 9401) of *Hylarana bannanica* in preservative. **A.** Dorsal view; **B.** Ventral view; **C.** Close-up view of the right side of the head; **D** Close-up view of the left side of the head. Photos by Dingqi Rao.

Dorsal skin slightly rough, upper lateral skin granular, lower lateral and ventral skin smooth; dorsolateral folds distinct, supratympanic fold absent; one white gland above base of forelimb behind tympanum on each side; some tiny tubercles form indistinct skin ridges on dorsal tibia.

In preservative, dorsum light brown, lateral side greyish-brown, ventral side of head and limbs yellowish-white, belly greyish-white, iris black, pupil white.

Distribution. Currently, *Hylarana bannanica* is known to be distributed in Xishuangbanna Prefecture, Yunnan Province, China, as well as northern Laos (Phongsaly Province), Thailand (Chanthaburi, Ubon Ratchathani, Amnat Charoen, Sa Kaeo, Prachin Buri, Nakhon Ratchasima and Chachoengsao provinces), southwest Cambodia (Cardamon Mountains) and peninsular Myanmar (Tanintharay Region), based on data from Rao and Yang (1997), Chuaynkern et al. (2004), Stuart and Emmett (2006), Yang and Rao (2008), Poyarkov et al. (2021), Zug and Mulcahy (2020), Zug (2022) and this study.

Conservation status. Further research is required to clarify the extent of the distribution, population size, trends and conservation status of the species. *Hylarana bannanica* is distributed over a large area including many protected areas. Across its range, the species seems not to be rare. Thus, we tentatively suggest *Hylarana bannanica* be considered a Least Concern (LC) species, following the IUCN's Red List Categories (IUCN Standards and Petitions Committee 2019).

Discussion

Dubois (1992) partitioned the genus *Rana* into many sections, one of which is the section *Hylarana*, which contains two subsections, namely subsection *Hydrophylax* and subsection *Hylarana*. He treated *Hydrophylax* as a subgenus and put it together with the newly-erected subgenera *Amnirana*, *Humerana*, *Papurana*, *Pulchrana* and *Sylvirana*

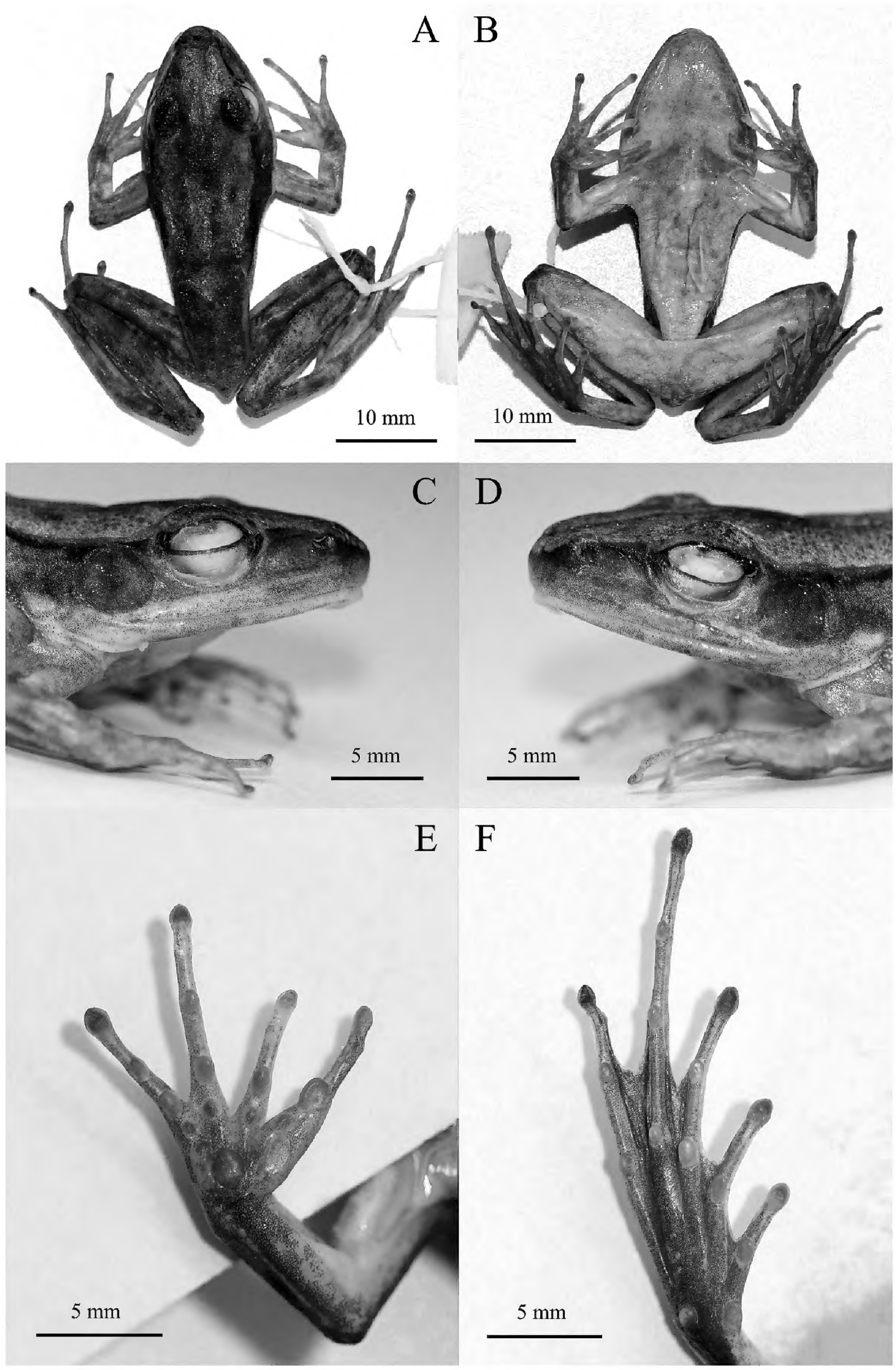

Figure 4. The topotypic specimen (KIZ2019BN) of *Hylarana bannanica* in preservative. **A** Dorsal view; **B** Ventral view; **C** Close-up view of the right side of the head; **D** Close-up view of the left side of the head; **E** Close-up view of the left palm; **F** Close-up view of the left sole. Photos by Shuo Liu.

in the subsection *Hydrophylax* and treated *Clinotarsus*, *Glandirana*, *Hylarana*, *Odorrana* and *Pterorana* as subgenera and put them together with the newly-erected subgenera *Chalcorana*, *Eburana*, *Nasirana*, *Sanguirana* and *Tylerana* in the subsection *Hylarana* and explicitly stated that these arrangements were preliminary hypotheses (Dubois 1992). Oliver et al. (2015) revised *Hylarana* sensu lato by utilising an inclusive molecular phylogeny, elevated *Amnirana*, *Chalcorana*, *Hydrophylax*, *Hylarana*, *Humerana*, *Papurana*, *Pulchrana* and *Sylvirana* to genus rank and erected two new genera, namely *Abavorana* and *Indosylvirana*. Chan et al. (2020) performed a comprehensive analysis of *Hylarana*

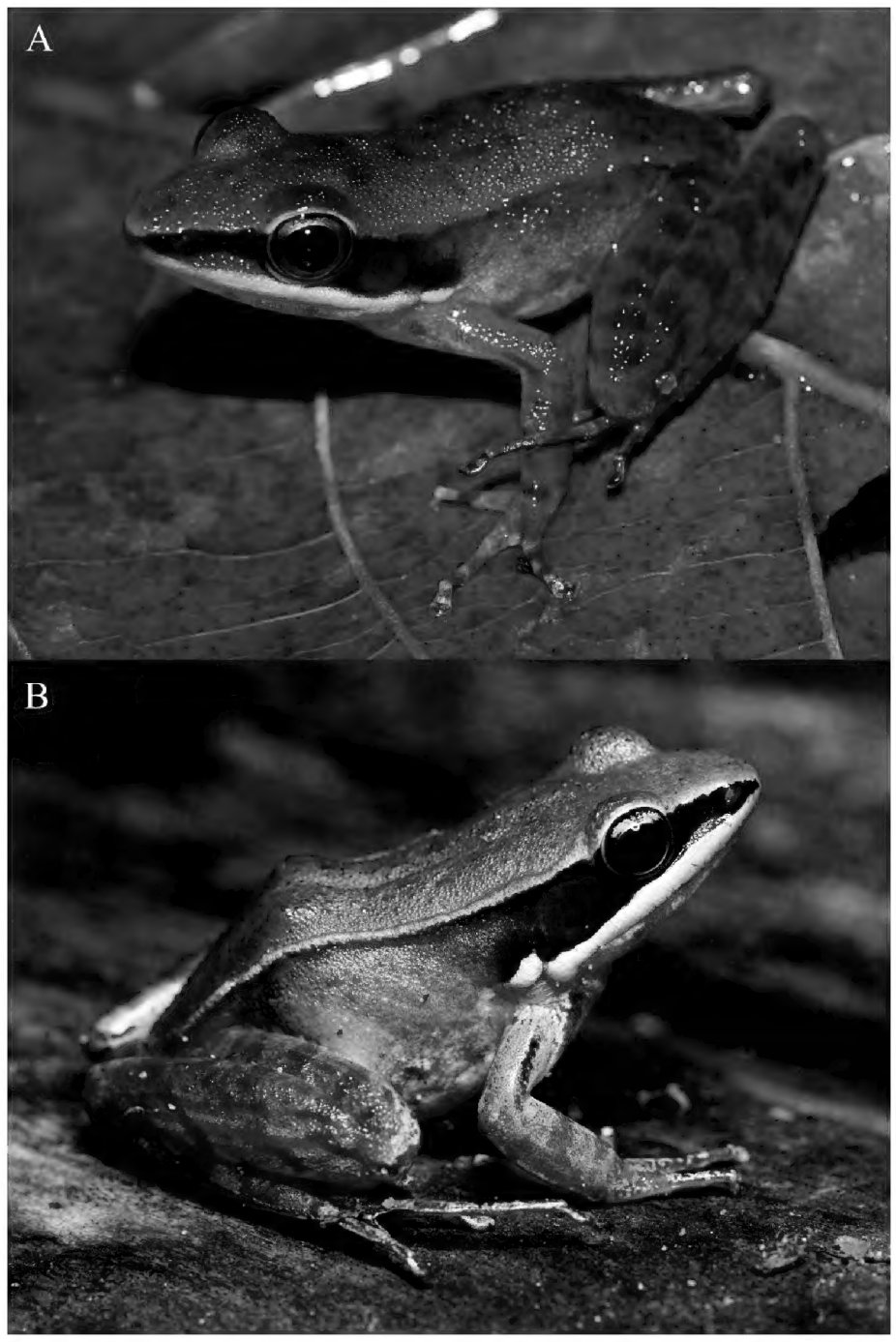

Figure 5. Comparison between *Hylarana bannanica* (**A** from Chanthaburi, Thailand) and *H. milleti* (**B** from Bidoup-Nui Ba, Lam Dong, Vietnam) in life. Photos by Parinya Pawangkhanant (**A**) and Nikolay A. Poyarkov (**B**).

sensu lato and also recognised the ten genera *Abavorana*, *Amnirana*, *Chalcorana*, *Hydrophylax*, *Hylarana*, *Humerana*, *Indosylvirana*, *Papurana*, *Pulchrana* and *Sylvirana* in it. Later, Dubois et al. (2021) found *Chalcorana* to be paraphyletic with *Pulchrana* and *Amnirana* and *Sylvirana*, *Papurana*, *Hydrophylax*, *Hylarana* and *Indosylvirana* to be polyphyletic; therefore, they placed all of the genera within *Hylarana* sensu lato, except for *Abavorana*, into the synonymy of *Hylarana*. However, we consider that these synonymous genera may be valid and need to be resurrected, at least for some of them. For example, Dubois et al. (2021) recovered *Sylvirana* to be polyphyletic due to *Sylvirana guentheri* as the sister taxon of *Humerana miopus*. In our phylogenetic analysis, *Hylarana guentheri* was also nested in the subgenus *Humerana* with strong support. Nevertheless, we cannot say directly that *Sylvirana* or *Humerana* is invalid, unless *Hylarana guentheri* is the type species of *Sylvirana*. *Hylarana guentheri* is a very common species in southern China and northern-central Vietnam and we have collected specimens of this species multiple times. This species has a large body size, which is different from most species of the subgenus *Sylvirana* and consistent with most species of the subgenus *Humerana*. Since *Hylarana guentheri* is not the type species of *Sylvirana*, therefore, we consider that *Hylarana guentheri* should be moved to *Humerana* from *Sylvirana*, and *Sylvirana* and *Humerana* are still valid, instead of synonymising them. Anyway, we still adopt the current arrangement (Dubois et al. 2021; Frost 2023) of *Hylarana* sensu lato for the time being; further morphological and molecular studies are required to elucidate the division of genera within *Hylarana* sensu lato.

Hylarana bannanica was described from Xishuangbanna, Yunnan, China, in 1997 and no new specimens from its type locality have been reported since then. The specimen (KIZ2019BN) we collected is the first rediscovery from the type locality of this species since it was described more than 20 years ago. Unfortunately, this specimen was misidentified as a subadult of the local common species *H. cubitalis* (Smith, 1917) and was not taken seriously when it was collected, so that the habitat information at the collection site and photos of this specimen in life were not recorded. In the subsequent process of specimen sorting, we discovered that this specimen is an adult male due to the presence of nuptial pad and vocal sacs, but without a large oval gland on the inner side of each elbow, which shows it is obviously not *H. cubitalis*, so we conducted a detailed study on this specimen. This experience reminds us that it is necessary to have sufficient taxonomic competence when doing fieldwork and that those who visit different locations should be aware of what species are distributed or what species may be distributed there.

In previous studies (e.g. Frost et al. (2006); Oliver et al. (2015); Chan et al. (2020); Dubois et al. (2021); Reilly et al. (2022)), *Hylarana milleti* (Fig. 5B) was once placed in the genera or subgenera *Sylvirana*, *Indosylvirana* and *Papurana*, respectively. In our phylogenetic analysis, it is evident that *H. milleti* and *H. bannanica* are not conspecific, but their phylogenetic positions within the genus have not been resolved. At present, we cannot determine which subgenus these two species belong to respectively. The systematic relationship within this genus needs to be further resolved.

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